

[1] X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RA MEDLINE:99238303; PUBMED:10220315;
 RA Etlanger M.A., Wachter R.M., Hanson G.T., Kallio K., Remington S.J.;
 RT *Structural and spectral responses of green fluorescent protein
 RT variants to changes in pH*;
 CC BIOCHEMISTRY 38:1828-1830(1999)
 CC CC
 CC BLUE CHEMILUMINESCENCE OF THE PROTEIN AQUORIN INTO GREEN
 CC FLUORESCENT LIGHT BY ENERGY TRANSFER. FLUORESCES IN VIVO UPON
 CC RECEIVING ENERGY FROM THE CA(2+)-ACTIVATED PHOTOPROTEIN Aequorin.
 CC ABSORBS LIGHT MAXIMALLY AT 395 NM AND EXHIBITS A SMALLER
 CC ABSORBANCE PEAK AT 470 NM. THE FLUORESCENCE EMISSION SPECTRUM
 CC IS IDENTICAL WITH A SHOULDER AT 540 NM.
 CC -1- SUBUNIT: MONOMER
 CC -1- TISSUE SPECIFICITY: PHOTOCYTES.
 CC -1- PTM: CONTAINS A COVALENTLY ATTACHED CHROMOPHORE, WHICH IS COMPOSED
 CC OF MODIFIED AMINO ACID RESIDUES. THE CHROMOPHORE IS FORMED UPON
 CC CYCLIZATION OF THE RESIDUES SER-DEHYDROTYR-GLY.
 CC -1- BIOCHEMISTRY: has become a useful and ubiquitous tool for making
 CC functional fusion proteins. It is used to study the localization of
 CC functions as a fluorescent protein tag. GFP tolerates N- and C-
 CC terminal fusion to a broad variety of proteins. It has been
 CC expressed in bacteria, yeast, slime mold, plants, drosophila,
 CC zebrafish, and in mammalian cells. As a noninvasive fluorescent
 CC marker in living cells, it allows for a wide range of applications
 CC including gene expression, cell fate determination, and gene
 CC expression or as a measure of protein-protein interactions.
 CC -1- DATABASE: NAME-Protein Spotlight;
 CC NOTE-Issue 11 of June 2001;
 CC WWW="http://www.expasy.org/spotlight/articles/spot101.html".
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 CC or send an email to license@isb-sib.ch).
 CC EMBL: M52654; AAA27722.1;
 CC DR EMBL: M52653; AAA27721.1;
 CC DR EMBL: L29345; AAM58246.1;
 CC DR PDB: 1GFL; 11-JAN-97.
 CC DR PDB: 1EMK; 20-AUG-97.
 CC DR PDB: 1EMK; 16-JUN-97.
 CC DR PDB: 1EMK; 20-AUG-97.
 CC DR PDB: 2EMO; 20-AUG-97.
 CC DR PDB: 1EME; 20-AUG-97.
 CC DR PDB: 1EMP; 20-AUG-97.
 CC DR PDB: 1EMK; 20-AUG-97.
 CC DR PDB: 1EMK; 20-AUG-97.
 CC DR PDB: 1EMK; 20-AUG-97.
 CC DR PDB: 2EMK; 20-AUG-97.
 CC DR PDB: 2EMO; 20-AUG-97.
 CC DR PDB: 1PFP; 07-JUL-97.
 CC DR PDB: 1PFP; 07-JUL-97.
 CC DR InterPro: IPR000786
 CC DR Pfam: PF01353; GFP: 1, Green_fl_protein.
 CC DR PRINTS: PR01229; GFP: 1, Green_fl_protein; 1.
 CC DR ProDom: PD013756; Green_fl_protein; 1.
 CC DR Luminescence; 3d-structure.
 CC KW SAEANT 167
 CC FT VARIANT 108 108 T->S;
 CC FT VARIANT 141 141 L->M.
 CC FT VARIANT 219 219 V->I.
 CC FT H->Q (IN REF. 2).
 CC FT CONFLICT 125 125 H->Q (IN REF. 2).
 CC FT CONFLICT 157 157 Q->P (IN REF. 2).
 CC FT CONFLICT 177 177 E->G (IN REF. 2).
 CC FT SEQUENCE 238 AA; 26886 MA; EAA56211FF66603 CHC64;
 CC SQ

Query Match 97 98; Score 1247; DB 1; Length 238;
 Database Similarity 98 38; Pct. M. 111 99;
 Matches 234; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 VSGKEGFTGVVPLVVELDGDVNGKFSVSGEGEDATYKLTFTCTTGKLPVPPMPL 61
 DB 1 MSSEGLFTGVVPLVVELDGDVNGKFSVSGEGEDATYKLTFTCTTGKLPVPPMPL 60
 QY 62 VTTLSVGVQCSRVPYDHHKHQDFPKSAMPEGYQERTIPFDKGNKTRAYKFGDGLV 121
 DB 61 VTTLSVGVQCSRVPYDHHKHQDFPKSAMPEGYQERTIPFDKGNKTRAYKFGDGLV 120
 QY 122 NRIELKIGDFEDNLTGLHKLKLYVNNHNVYIMADOKNKKYKFIHNNIDGVSQJAD 181
 DB 121 NRIELKIGDFEDNLTGLHKLKLYVNNHNVYIMADOKNKKYKFIHNNIDGVSQJAD 180
 QY 182 HYQONTPIGDGVPVLLPDHNLSTGSAISKDPNEKRHHVLLGFTVAGTILGNDELK 239
 DB 181 HYQONTPIGDGVPVLLPDHNLSTGSAISKDPNEKRHHVLLGFTVAGTILGNDELK 238
 RESULT 2
 SYLV-HAETIN STANDARD: PRT: 861 AA.
 ID PVL-HAETIN
 AC P43827; 1995 (Ref. 32, Created)
 DT 01-NOV-1995 (Ref. 32, Sequence update)
 DT 15-JUN-2002 (Ref. 41, Last annotation update)
 DE Leucyl-tRNA synthetase (SC 6.1.1.4) (Leucine-tRNA ligase) (LeuRS).
 GN LEUS OR H10921.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 OC Haemophilus influenzae.
 CC NCBI_TaxID=727;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN-Rd / KW20 / ATCC 51907;
 RX MEDLINE:95350630; PUBMED:7542800;
 RA Kerkovander R., Ruit C.J., Tomij J.-P., Doughterty B.A., Merriest J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shitley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E.C., Cotton M.C.,
 RA Otterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Georgagen N.S.W.,
 RA Kerkovander R., McDonald L.A., Small K.V., Fraser K.M., Smith H.O.,
 RA Venter J.C.;
 RT RT Rd.*
 RT Science 269:496-512(1995).
 RL -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
 RL L-leucyl-tRNA(Leu) + H2O.
 RL -1- SUBUNIT: MONOMER (HOMOTETRAMER).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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 CC EMBL: U02774; AAC22481.1;
 CC TIGR: H10921;
 CC InterPro: IPR002302; Leu-tRNA-synt.1a.
 CC InterPro: IPR002300; tRNA-synt.1a.
 CC InterPro: IPR001412; tRNA-synt.1.
 CC Pfam: PF00133; tRNA-synt.1; 1.
 CC TrEMBL: P00003; tRNA-synt.1.
 CC TrEMBL: U02774; tRNA-synt.1.
 CC PROSITE: P500178; AA_TRNA_LIGASE_I; 1.

KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 Complete proteome.
 FT SITE 42 52 *HIGH* REGION.
 FT SITE 619 623 *KMSK* REGION.
 FT SITE 622 622 ATP (BT SIMILARITY)
 SQ SEQUENCE 861 AA; 97750 MW; 2893304684CB87 CRC64;
 Query Match 7.2%; Score 91.5; DB 1; Length 861;
 Best Local Similarity 24.1%; Pred. No. 3.6;
 Matches 46; Conservative 26; Mismatches 60; Indels 59; Gaps 11;
 OY 50 TTGKLPVWPLVTLTSLVSGVCFSRVDFRMKHQDFKSAMPEGVQERTIFPKD----- 103
 DB 314 TGDCLPV-WVANEFLVHGTCGAVNAVPAH-DQDDE-----EFAQKSLPIKQVIAPLA 364
 OY 104 DQNYKTRAEKFGEDTLVNRLEIKGIDFKEDGILGHKLEYNYNSHNYIADK-ORNGI 162
 DB 365 DEEDILTKQAFVEHGLKGVNSDFDQNF--DGAFNG-----IDKLEKLEGV 408
 OY 163 ---KYNKIRH-----NEDGSVOLADHVQNTPTGDCPVLPDNRHLY- 202
 DB 409 GKQVNVRLADGVSQRYSYWGAPITPLTLENGDVPA-----PMEDPIILPDRVMD 461
 OY 203 STQSALKSDPN 213
 DB 462 GVKSPINADPN 472
 RESULT 3
 SYL XLYFA STANDARD: PRT: 879 AA.
 AC Q9P8G:
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 GN LEUS OR XF2176
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
 OC Xylella.
 OX NCBI_TaxID=2371;
 RP SEQUENCE FROM N.A.
 RC STRAIN=9a5c;
 RX MEDLINE=20365717; PubMed=10910347;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Barroga M.H., Alves L.C.S., Araya J.E., Baia G.S., Baptista C.S.,
 RA Barros M.H., Bonaccorsi E.D., Bordin J.E., Borek J.R., Borek S.H.,
 RA Coutinho L.L., Colombo C., Costa F.F., Costa M.C.R., Costa Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorcy H.,
 RA Pacinani A.P., Pereira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
 RA Garier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.R.,
 RA Ho P.L., Hohnselt J.D., Junqueira M.E., Kemper E.L., Khalilima A.P.,
 RA Kleges E.G., Krumholz L., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.D.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Raimieri D., Azeiteiro J.B.,
 RA de Alencar E.B., Roberto P.G., Rodrigues V. de Rosa A.J.M.,
 RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
 RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.H.,
 RA de Souza A.P., Terenzi M.P., Truffi D., Tsai S.M., Tsuchioka M.H.,
 RA Valada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Zechin J., Zechin J., Zechin J., Zechin J.,
 RA Nature 406:131-159(2000).

CC -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) - AMP +
 CC phosphate + L-leucyl-CRNA(Leu).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO CLASS: L-AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -1- SIMILARITY: BELONGS TO CLASS: L-AMINOACYL-TRNA SYNTHETASE FAMILY.
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 CC EMBL: AE004031; AAF84975.1; ALT-INIT.
 DR InterPro: IPR002302; Leu-TRNA-syntLa.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR Pfam: PF00395; TRNA-SYNTHASE.
 DR PROSITE: TIGR00396; leus.bact.1.
 DR PROSITE: PS00178; AA-TRNA-LIGASE.1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 45 55 *HIGH* REGION.
 FT SITE 630 640 ATP (BY SIMILARITY).
 SQ SEQUENCE 879 AA; 95796 MW; 9FDCB952092919E CRC64;
 Query Match 7.0%; Score 89.5; DB 1; Length 879;
 Best Local Similarity 22.2%; Pred. No. 5.4;
 Matches 44; Conservative 29; Mismatches 68; Indels 57; Gaps 10;
 OY 50 TTGKLPVWPLVTLTSLVSGVCFSRVDFRMKHQDFKSAMPEGVQERTIFPKDQNY- 107
 DB 321 TNEOLPV-WVANEFLVHGTCGAVNAVPGHDQDQDF-ANKYGLPIQVIALKPKNQDE 377
 OY 108 -----TTRAEVFEGEDTLVNRLEIKGIDFKEDGILGHKLEYNYNSHNYI 153
 DB 378 STWEPDWDHMYADTR---EFE---LINSAGFDGLDYDAFVLAERF----- 421
 OY 154 MADKQNG-IVKFKIRHNIEDGSVOLADHVQNTPT-----GDGPVLLPN 199
 DB 422 ---RQGRGQRRVYRLR---DMGVSQRYSYWGAPITPTGCGAVPVPDQVLPILPN 474
 OY 200 -HYLSYQSALKSDPNKRR 216
 DB 475 VAFSGTQSPKIDFENRR 492
 DPOE YEAST
 ID DPOE YEAST STANDARD: PRT: 2222 AA.
 AC P21951; 991 (Rel. 19, Created)
 DT 01-NOV-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE DNA polymerase epsilon, catalytic subunit A (BC 2.7.7) (DNA
 DE polymerase II subunit A).
 GN POL2 OR DUN2 OR YNL262W OR N0825.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetes; Saccharomycotina; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1214-1221.
 RX MEDLINE=90381771; PubMed=2169349;
 RA Morrison A., Araki H., Clark A.B., Hamatake R.K., Sugino A.;
 RF A third essential DNA polymerase in *S. cerevisiae*.;
 RL Cell 62:1143-1151(1990).
 RP SEQUENCE OF 1-2221 FROM N.A.
 RC STRAIN=S288c / FY1679;
 RX MEDLINE=96310631; PubMed=8740425;

RA Sen-Gupta M., Lyck R., Fleig U., Niedenthal P.K., Hegemann J.H.;
 RT "The sequence of a 24,152 bp segment from the left arm of chromosome
 RT XIV from Saccharomyces cerevisiae between the BNI1 and the POL2
 RT genes";
 RT Yeast 12:905-514(1996).
 RN [3]
 RN [3] DEPENDANT SENSITIVE MUTANTS
 RX MEDLINE=92164563; PubMed=153745;
 RA Araki H., Ropp P.A., Johnson A.L., Johnston L.H., Morrison A.,
 RA Sugino A.;
 RT "DNA polymerase II, the probable homolog of mammalian DNA polymerase
 RT epsilon, replicates chromosomal DNA in the yeast Saccharomyces
 RT cerevisiae";
 RT Nucleic Acids Res. 21:713-740(1993).
 CC [1]- FUNCTION: DNA POLYMERASE II PARTICIPATES IN CHROMOSOMAL DNA
 CC REPLICATION.
 CC [1]- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + [DNA(N)].
 CC [1]- SUBUNIT: CONSISTS OF FIVE SUBUNITS (200 kDa, 80 kDa, 34 kDa, 30
 CC kDa, AND 29 kDa); ION: NUCLEAR.
 CC [1]- DOMAIN: THE DNA POLYMERASE ACTIVITY DOMAIN RESIDES IN THE
 CC N-TERMINAL HALF OF THE PROTEIN, WHILE THE C-TERMINUS IS NECESSARY
 CC FOR COMPLEXING SUBUNITS B AND C.
 CC [1]- MISCELLANEOUS: IN EUKARYOTES THERE ARE FIVE DNA POLYMERASES:
 CC ALPHA, BETA, GAMMA, DELTA, AND EPSILON WHICH ARE RESPONSIBLE FOR
 CC DNA REPLICATION, REPAIR, AND RECOMBINATION.
 CC [1]- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY. HIGH
 CC SIMILARITY WITH MAMMALIAN DNA POLYMERASE EPSILON.
 CC
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 CC
 CC EMBL: M5046; CA89711.1;
 CC DR EMBL: M5046; CA89711.1;
 CC DR EMBL: 271338; CA96169.1;
 CC DR PIR: A36028; A36028.
 CC DR SGD: S0005206; POL2.
 CC DR InterPro: IPR002064; DNA_POL.B.
 CC DR Pfam: PF00136; DNA_POL.B.1.
 CC DR SMART: SM00486; DNA_POL.B.
 CC DR SMART: SM00486; DNA_POL.B.
 CC KW PROSITE: PS00116; DNA POLYMERASE B; FALSE NEG.
 CC KW Transferrase; DNA-directed DNA polymerase; DNA replication;
 CC KW DNA-binding; Zinc-finger; Nuclear protein.
 CC KW ZM_FING 2108 2181 POTENTIAL.
 CC FT VARIANT 544 544 M -> I (IN POL2-9 TS MUTANT).
 CC FT VARIANT 710 710 M -> S (IN POL2-18 TS MUTANT).
 CC SQ SEQUENCE 2222 AA, 255669 MW, CRODDEZNLK47DQ58 CWC64.
 CC
 CC Query Match 6.9%; Score 87.5; DB 1; Length 2222;
 CC Best Local Similarity 28.2%; Pred. No. 25;
 CC Matches 37; Conservative 14; Mismatches 49; Indels 31; Gaps 7;
 CC
 CC 54 LEVWPP-TLTVLSYGVQCFSRYPDHM-----KHDFPKSMPEGVY---QERTI 99
 CC 883 LPASFPETVFTLENGKXILSYSPCMUNYRHKQFTNHQYQELKPLNYIYHSENTI 942
 CC 100 FFKDDQNTKYR-AEYKVEGDTLVNR-----IELGIDFKEDGMILGHLENYN 147
 CC 943 FFEVQGYPKAMILPSSKEGKTKKRVAFVNEGDSLAKGFLKRRGEL---OLIKNFO 999
 CC 148 S---HNYITMAD 156
 CC 1000 SDIFKVFLEGD 1010

RESULT 5

SIAP_BACLI
 ID SLAP_BACLI STANDARD: PRT: 874 AA.
 AC P49052;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 OS Saccharomyces cerevisiae (Surface layer protein).
 CS Bacillus licheniformis
 CS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CC NCBI_TaxID=1402;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=NM-9708565; PubMed=8964497;
 RC Zhu X., Kevlish R.R., Malathi P., Ghosh B.K.;
 RA "The complete nucleotide sequence of the Bacillus licheniformis NM105
 RT S-layer-encoding gene";
 RT Gene 173:189-194(1996).
 RL [1]- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
 CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
 CC [1]- SIMILARITY: CONTAINS 3 S-LAYER HOMOLOGY (SLH) DOMAINS.
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 CC
 CC EMBL: U38842; AAC44405.1;
 CC DR InterPro: IPR001119; SLH.
 CC DR PIR: A00139; SLH.
 CC KW Signal; Cell wall; S-layer; Repeat.
 CC FT SIGNAL 1 30 POTENTIAL.
 CC FT CHAIN 31 874 S-LAYER PROTEIN.
 CC FT DOMAIN 33 93
 CC FT DOMAIN 34 137 SLH 1.
 CC FT DOMAIN 35 157 SLH 2.
 CC FT DOMAIN 36 177 SLH 3.
 CC SQ SEQUENCE 874 AA; 92734 MW; EFADCAIFF27D32AF CWC64;
 CC
 CC Query Match 6.8%; Score 87; DB 1; Length 874;
 CC Best Local Similarity 22.8%; Pred. No. 8.8;
 CC Matches 65; Conservative 28; Mismatches 96; Indels 96; Gaps 14;
 CC
 CC 6 EELF--TGVVPLI---VELDQVNGHKFSVSGECDAI-----YKLTLEKI 48
 CC 551 KEVFPQGVVAVLDVTTTNEGSIQTSSIRKGVNKGATGTHFQPNASGEGYSLHVEVT 610
 CC 49 CTIGKLVFWPTLV-----TTLSYGVQCFSRYPDHMKHOFKSNMPEGYQOER 97
 CC 611 KSNICHARPLELIVSAQAGKADITLQAGNVAVLSNFTTEGVTAADADLAGT--EP 668
 CC 98 TIFPKDQSNYKTRAEVKEGDTLVNRLEKGD--FKEDGMILGHLENYNHSNYLM 154
 CC 669 RV-----GNDKI-ASAKLEGTAKVTKGTAGVDTVLTKDGTAGH-ATITVTQNTQIT 721
 CC 155 ADNQK-----NGIKVNFKIRN-----IEDGSVQLAHD 182
 CC 722 SVAFKVEVQFQENREVWIDVLDVYKSDKDVLSKLNLSIEHVRIVDECTEQ---- 777
 CC 183 YQNTPTPGVPLPDNHLISFOSALS KDPNKRQHVLLGFTVA 227
 CC 778 -----GKV-----YLDNRNDAITFDND-----VALGYVTA 802
 CC
 CC RESULT 5
 CC CP51_CANGA
 ID CP51_CANGA STANDARD: PRT: 533 AA.
 AC P50859; 002312;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Cytochrome P450 51 (EC 1.14.14.-) (CYP51) (P450-LI1A1) (Sterol 14-
 OM demethylase) (lanosterol 14-alpha demethylase) (P450-14DM).
 GN ERG1 OR Y0757
 OS Candida glabrata (Yeast) (Torulopolis glabrata).
 CC Sukayoka; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 ON NCBI_TaxID=5478;
 RX [1] JENCKS FROM N.A.
 RC STRAIN=2001-15.
 DE MEDLINE=96161286; PubMed=8593007;
 RA Geber A., Hitchcock C.A., Swartz J.E., Pullen F.S., Marsden K.E.,
 Kwon-Chung K.J., Bennett J.E.;
 RT "Deletion of the Candida glabrata ERG3 and ERG11 genes: effect on cell
 RT viability, cell growth, sterol composition, and antifungal
 RT susceptibility.";
 RT J. Antimicrob. Agents Chemother. 39:2708-2717(1995).
 RN [2]
 RP SEQUENCE OF 60-473 FROM N.A.
 RC STRAIN=ATCC 2001;
 RX MEDLINE=95081364; PubMed=7989540;
 RA Burgener-Kaluz P., Kuber J.P., Buchman T.G., Bille J.,
 Rosier M.;
 RT "Molecular detection and identification of Candida albicans and
 RT Candida glabrata by polymerase chain reaction of a cyclochrome P-450
 RT species-specific nested PCR amplification of a cyclochrome P-450
 RT lanosterol-alpha-demethylase (LI1A1) gene fragment.";
 RL J. Clin. Microbiol. 32:1902-1907(1994).
 CC [-] FUNCTION: CATALYZES C14-DEMETHYLATION OF LANOSTEROL WHICH IS
 CC CRITICAL FOR ERGOSTEROL BIOSYNTHESIS. IT TRANSFORMS LANOSTEROL
 CC INTO 4,14-DIMETHYRYL CHOLESTRA-8,14,24-TRIENE-3-BETA-OL
 CC
 CC [-] PATHWAY: Ergosterol biosynthesis.
 CC [-] SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
 CC
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 CC
 DR EMBL; L40389; AB02329.1;
 DR EMBL; S75389; AB023679.1;
 DR EMBL; U001116; Cyclochrome P450.
 DR PRINTS; PR00385; P450.
 DR PROSITE; PS00086; CYTOCHROME_P450; 1.
 KW ELECTRON transport; Oxidoreductase; Monooxygenase; Membrane; Heme;
 KW Sterol biosynthesis.
 FT BINDING 472 472 HEME (BY SIMILARITY).
 FT CONFLICT 64 64 I -> M (IN REF. 2).
 FT CONFLICT 41 41 I -> M (IN REF. 1).
 FT SEQUENCE 533 AA; 61305 MW; A0506C17507562F7 CRC64;
 Query Match 6.88; Score 86.5; DB 1; Length 533;
 Best Local Similarity 21.48; Pred. No. 5.3;
 Matches 44; Conservative 32; Mismatches 81; Indels 49; Gaps 8;
 QY 25 GHRFSVS---GGEGDANYGKLFKIFCTYTGKLPFWPVTIVTLTSGVCSFRPDH--M 79
 DB 109 GHEFTNKLADVSNAEYSIL-----TIPTFKGVYDCPNHRLA 149
 QY 80 QKHDFKSA--PEGYV-----QRTTFKDCGNTKRAEVKFGDVLNRIKLGDF 131
 DB 150 EKKFPYKALTEAFYRVYVLAIEETKYFRNSKFNKINNSGIVDMVQSPDM--TIF 207
 QY 132 EKDNTLGHKLEYNNSHWYTMADKNGKINVKFKIRNIDEGSVQADHYQNTFPGD 191
 DB 208 TASSRLKGEKRDLDLDTFALLSDLDKGPPIINF-VFPNLPLEYRKHDAQAALS---- 263
 QY 192 GPVLLPDNHYLSTQSALSROPNEKRD 217
 DB 264 -----GTTNSLIEREKND 278
 RESULT 7
 ID D152_HAETIN STANDARD; PRT; 795 AA.
 AC P44935; 1995 (Rel. 32, Created)
 RI 01-NOV-1995 (Rel. 32, Last annotation update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Protective surface antigen D15 precursor (80 kDa D15 antigen)
 DE (D-15-Ag) (Outer membrane protein D15).
 GN HI0917.
 OS Haemophilus influenzae.
 CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 CC Haemophilus influenzae.
 ON NCBI_TaxID=727;
 RX NCBI_TaxID=727;
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 Kerlavage A.R., Bult C.J., Tomb J.-F., Fields C., Gocayne J.M.,
 Scott J.D., Shetty S., Li P., Blakesley R., Green R., Gill
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 Venter J.C.;
 RT "A whole-genome random sequencing and assembly of Haemophilus influenzae
 RT strain Rd.";
 RL Science 269:496-512(1995).
 CC [-] SUBCELLULAR LOCATION: Outer membrane.
 CC [-] SIMILARITY: BELONGS TO THE SURFACE ANTIGEN D15 FAMILY.
 CC
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 CC
 DR EMBL; U52773; AAC22575.1;
 DR EMBL; U001116; IPR000184; Bac.surfAq.D15.
 DR PRINTS; PR01103; Bac.surfAq.Ag.1.
 KW Antigen; Outer membrane; Signal; Complete proteome.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 795 PROTECTIVE SURFACE ANTIGEN D15.
 FT SEQUENCE 795 AA; 87478 MW; B85691FC2E6D4 CRC64;
 Query Match 6.88; Score 86.5; DB 1; Length 795;
 Best Local Similarity 21.94; Pred. No. 8.7; 78; Indels 63; Gaps 11;
 Matches 48; Conservative 30; Mismatches 30;
 QY 65 LSTGVGCVSFRPDHAKHDF-----FKSAMPEGYVQE-----RTI 99
 DB 427 IGTGTSIGTSIQASQKIDLVNRIKLGDFKDKNT---LGH-----KLEYNYS 148
 QY 100 EFKDDGNTKRAEVKFGDVLNRIKLGDFKDKNT---LGH-----KLEYNYS 148
 DB 487 EFTYDYSKSDTSKRTTYGNTVL-GPPVNNNSYVVLGHTKINSFALETN--- 542
 QY 149 INYITMADKQK-NGIKVNFKIRNIDEGSVQADHYTQQ-----NTPIGDGPVLL 196
 DB 543 NKITIOSMKFKNGIKTN-----DPFSFGWNNYSINRGVFTGKVASLG-GRVTI 593
 QY 197 P--DNHYLSTQSALSROPNEKRDHMLGVPTAGITLG 233

594 PGSDNKYYKLSADVQGFYPLDRDHLWVVSAKASAGYANG 632

594 PGSDNYKYLSDVQGVFLPDRLHLWYSAKASAGYANG 632

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RESULT 8
ID D151_HAEIN
AC 746024_1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DT DE Protective surface antigen D15 precursor (80 kDa D15 antigen)
DE (D-15-Ag) (Outer membrane protein D15).
DE Haemophilus influenzae.
CC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
CC Haemophilus.
CC 185_taxid=727;
RN 11
RN SEQUENCE FROM N.A.
RN STRAIN=Serotype B;
RN MEDLINE=95255676; PubMed=7737523;
RN Plack F.S., Loosmore S., Chong P., Thomas W.R.:
RN "The sequencing of the 90-kDa D15 protective surface antigen of
RN Haemophilus influenzae.,"
RN Gene 136:97-99(1995).
RN 121
RN SEQUENCE FROM N.A.
RN STRAIN=Minnia, and Eagan / Serotype B;
RN MEDLINE=97427952; PubMed=9284140;
RN Loosmore S.M., Yang Y.P., Coleman D.C., Shortt J.M., England D.M.,
RN Klein M.H.:
RN "The 90-kDa D15 protective surface antigen of Haemophilus
RN influenzae: a universal protective antigen against
RN invasive disease.,"
RN Infect. Immun. 65:3701-3707(1997).
RN 13
RN - SUBCELLULAR LOCATION: Outer membrane.
CC CC - SIMILARITY: BELONGS TO THE SURFACE ANTIGEN D15 FAMILY.
CC CC
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CC CC or send an email to license@ebi.ac.uk).
CC CC EMBL: U13961; AA856544.1;
CC CC EMBL: U60832; AA851974.1;
CC CC EMBL: U60833; AA851976.1;
CC CC InterPro: IPR000184; Bac_surfAg_D15.
CC CC Pfam: PF01103; Bac_surfaceAg; 1.
CC CC Antigen; Outer membrane; Signal.
CC CC SIGNAL: 1 19 POTENTIAL.
CC CC SHATH: 20 77
CC CC SEQUENCE 737 AA; 87675 MW; 2F93D5E3669A1B CIRC04;
CC CC
Query Match 6.8%; Score 86.5; DB 1; Length 797;
Best Local Similarity 21.9%; Prod. No. 8.7;
Matches 48; Conservative 30; Mismatches 78; Indels 63; Gaps 11;

65 LSYGVTSQVSRVQKQVQDNVLCGTGANSVINGTKDGFISNVLGYTFYFDKGVSGWV 485
427 IGVGVTSQVSRVQKQVQDNVLCGTGANSVINGTKDGFISNVLGYTFYFDKGVSGWV 485
100 PFKDQGNVATRVAFGGDTLVNRLKLGIDFKEDGNT---LGH---KLEYNVNS 148
487 FFENTDKSDTSISNRYKRTTGVSNVTLGPVNENNSYVYGLGHTYMKISIALEYN--- 542
149 HNVYIMADQKQ-NGIKVNFKIRHNIEDSGVQLADHTYQO---NTPIGDGPVLL 196
543 RNLIIYLSMKFNGKNGIKTN-----DDFSFQNTNSLNGVYFFYKGVKASLG-GRVTL 593
197 P-DHYLTLSQALSQPKNEKRDIKQVYLVFGVFTAGTILG 233

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594 PGSDNKKYKLSADVQGYPLDRDHLFVVSASAKASAGYANG 632

```

594 PSDNDKYYLSADVGDFPLDRDLRLWTYSKASAGIYANG 632

RESULT 9
ID TRMA_CANJE STANDARD; PRT; 357 AA.
09PDP2:
AC TT TRMA_CANJE IDW 41, Created)
DE DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE DE trNA (Uracil-5'-methyltransferase (EC 2.1.1.35) (tRNA(M-5-U54))-methyltransferase) (RUMT).
GN TRMA OR CJO831C.
CC Campylobacter jejuni.
CC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group; Campylobacter.
CC [1]_TaxID=197;
CC [1]_TaxID=197;
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RR MEDLINE=10688204;
RR PARKHILL J., Wren B.M., Mungall K.K., Ketley J.M., Churcher C., Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S., Jagels M., Karlyshev A.V., Moule S.V., Pallen M.J., Penn C.W., Rogers M.T., Rutherford K.M., Van Vleet A.H.M., Whitehead S., Barrett B.G.;
RR "The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.*";
RR Nature 403:665-668(2000).
RL -1- FUNCTION: Catalyzes the formation of 5-methyl-uridine at position 54 (M-5-U54) in all tRNA (by similarity).
CC CC -1- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + methylated tRNA.
CC CC -1- SIMILARITY: BELONGS TO THE RNA MSU METHYLTRANSFERASE FAMILY. TBMA SUBFAMILY.
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-----
EMBL; ALJ39076; CAB73096.1; InterPro; IPRO00051; SAM_bind. PROSITE; PS01230.1; TBMA.1. PROSITE; PS01231; TBMA.2; FALSE NEG. Transferase; Methyltransferase; DOMAIN 207 213
ACV_SITE 315 315 BY SIMILARITY.
SEQUENCE 357 AA; 422776 MW; CEC32834/CEE497 CRC64; Query Match 6.8%; Score 86; Db 1; Length 357; Best Local Similarity 24.8%; Pred. No. 3.6; Matches 30; Conservative 18; Mismatches 39; Indels 34; Gaps 5;
OY 80 KOHDFKSAMPEGYQVERITFFDNGNTKTAERVK--EGDTLV-----NRIELG 128
DY 14 EKHSIFKYKFETTKFOFKAPSKDKHKHTFRALSTFIHQNDTLFTAMPDSKKKIYYI 73
DY 129 IDPED-----GNLGHKLKVWNSHWYIMADKKGKIKVNFKRTHIE 173
DY 74 LDFADEKICAFNPRLLEVLRODNKAEL-----FGVEFLTTKOE--LSITLLYHNKE 125
OY 174 D 174
DY 126 D 126

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DE Protective surface antigen D15 precursor (80 kDa D15 antigen)
 DE (D-15-Ag) (Outer membrane protein D15).
 OS Haemophilus influenzae.
 OS Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 CC Haemophilus.
 CC NCBI_TaxID=727;
 CC SEQUENCE FROM N.A.
 RC STRAIN=PAK 12085;
 RC MEDLINE=97427952; PubMed=9284140;
 RX Loosemore S.M., Yang Y.P., Coleman D.C., Shortreed D.M.,
 RA Klein M.H.;
 RA "Outer membrane protein D15 is conserved among Haemophilus influenzae
 RA species and may represent a universal protective antigen against
 RA infection." *Journal of Infectious Diseases* 165:3701-3707 (1997).
 RA Infect.Immun. 65:3701-3707 (1997).
 CC -1 SURCELLULAR LOCATION: Outer membrane.
 CC -1 SIMILARITY: BELONGS TO THE SURFACE ANTIGEN D15 FAMILY.
 CC
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 CC
 CC EMBL: U06834; AAB61977.1; --
 CC InterPro: IPRO00184; Bac_surfAg_D15.
 CC Pfam: PF01103; Bac_surfAg; 1.
 CC Gene: Outer membrane; Signal.
 CC PIR: P12111; 1.
 CC CHAIN 20 793 POTENTIAL.
 CC SEQUENCE 793 AA; 87511 MW; 51BFDB203680A1A4 CRC64;
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 CC Query Match 6.7%; Score 85.5; DB 1: Length 793;
 CC Best Local Similarity 22.4%; Pred. No. 11;
 CC Matches 4; Conservative 28; Mismatches 79; Indels 63; Gaps 11;
 CC
 CC 65 LSYGVQCFSRPNKQKDPD-----FKSANPEGYQVE-----FTI 99
 CC 427 IGYGTSEGISQTSIKQDNFLGCAAVSIAGTKNDYGVSLGYTPYFTKGVSGUGNI 486
 CC 100 FPKDNGMYTAAVYFEGDTLVNRIELKIDFKEKGI---LGR-----KLEYNTNS 148
 CC 147 FETNDASQTSKTSNRTKTYIGSNVL-GFPNNSVYSGYGRYTKNSINFALEIN--- 542
 CC 149 HNYVTHADKQK-NGIKVYKIRHNHEDISVOLADIIYQQ-----NTPIDGQPVLL 196
 CC 543 RNLVYTSMFKFGNGIKTN-----DFDSEFGNNYNSLNGVYFTKGVKASL-GRVTI 593
 CC 197 P-DNHYLTQSALSQDPNKKRHHVLLGFPVTAAGITLG 233
 CC 594 PGSDNKTYIKLNDVCGYFPDIDRRHWYWSAKASATYANG 632
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 CC RESULT 12
 CC ITH3_MESAO
 CC ITH3_MESAO STANDARD; PRT; 886 AA.
 CC DP P97280;
 CC AC 15-JUL-1998 (Rel. 36, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
 CC DE 12-OCT-2003 (Rel. 40, Deleted)
 CC DE Inner-alpha-trypsin inhibitor heavy chain H3 precursor (ITI heavy
 CC chain H3) (HC3).
 CC ITH3.
 CC GN Muscicula auratus (Golden hamster).
 CC OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mus; Mus musculus.
 CC NCBI_TaxID=10036;
 CC SEQUENCE FROM N.A.
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 CC ITH3_MESAO
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 CC DP P97280;
 CC AC 15-JUL-1998 (Rel. 36, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
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 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mus; Mus musculus.
 CC NCBI_TaxID=10036;
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 CC ITH3_MESAO STANDARD; PRT; 886 AA.
 CC DP P97280;
 CC AC 15-JUL-1998 (Rel. 36, Created)
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 CC chain H3) (HC3).
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 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mus; Mus musculus.
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 CC AC 15-JUL-1998 (Rel. 36, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
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 CC Mus; Mus musculus.
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 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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 CC ITH3_MESAO STANDARD; PRT; 886 AA.
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 CC AC 15-JUL-1998 (Rel. 36, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
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 CC GN Muscicula auratus (Golden hamster).
 CC OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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 CC ITH3_MESAO STANDARD; PRT; 886 AA.
 CC DP P97280;
 CC AC 15-JUL-1998 (Rel. 36, Created)
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 CC chain H3) (HC3).
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 CC GN Muscicula auratus (Golden hamster).
 CC OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 CC Mus; Mus musculus.
 CC NCBI_TaxID=10036;
 CC SEQUENCE FROM N.A.
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 CC ITH3_MESAO
 CC ITH3_MESAO STANDARD; PRT; 886 AA.
 CC DP P97280;
 CC AC 15-JUL-1998 (Rel. 36, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
 CC DE 12-OCT-2003 (Rel. 40, Deleted)
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 CC chain H3) (HC3).
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 CC ITH3_MESAO STANDARD; PRT; 886 AA.
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 CC ITH3_MESAO
 CC ITH3_MESAO STANDARD; PRT; 886 AA

